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☐	L35	L34 and l26	383
☐	L34	L33 and l6	3584
☐	L33	l1 and l2 and l32 and l4 and l19 and l20	5301
☐	L32	virus or bacteria or fungi or parasite	441078
☐	L31	l29 and L30	34
☐	L30	unmethylated	2939
☐	L29	L28 and l27	371
☐	L28	treat$ or prevent$ or ameliorat$	7744059
☐	L27	l23 and L26	373
☐	L26	$acgt$	8269
☐	L25	l23 and L24	6
☐	L24	tgacgtt or acgtt	142
☐	L23	L22 and l6	3551
☐	L22	l1 and l2 and l3 and l4 and l19 and l20	5136
☐	L21	l1 and l2 and l3 and l4 and l19 and l20	5136
☐	L20	synthesis or synthesized	680673
☐	L19	phosphorothioate	20777
☐	L18	@ay>=1980<=1994	11130613
☐	L17	@py>1994	18146165
☐	L16	L15 and l6 and l9	4114
☐	L15	l1 and l2 and l3 and l4 and l5	6260
☐	L11	cpg adj motif	537
☐	L10	(cg adj motif) or ((c adj g) adj5 motif)	68
☐	L9	carrier or pharmaceutical	1772082
☐	L8	oral or subcutaneous or intravenous or parenteral or transdermal	371417
☐	L7	sterol or cholesterol	86421
☐	L6	lipid or cationic adj lipid	121172
	L5	phosphorothioate or phosphoramidate or phosphotriester or	28924

☐		methylphosphonate	
☐	L4	stabilized or stabilization or modified or modification	2764354
☐	L3	cancer or tumor or tumour	305699
☐	L2	anti adj sense	27620
☐	L1	nucleic adj acid or nucleic adj acids or oligonucleotide or oligonucleotides	236260

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NEWS 15	DEC 18	MARPAT to CA/CAplus accession number crossover limit increased to 50,000
NEWS 16	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS 17	DEC 27	CA/CAplus enhanced with more pre-1907 records
NEWS 18	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS 19	JAN 16	CA/CAplus Company Name Thesaurus enhanced and reloaded
NEWS 20	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS 21	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS 22	JAN 22	CA/CAplus updated with revised CAS roles
NEWS 23	JAN 22	CA/CAplus enhanced with patent applications from India
NEWS 24	JAN 29	PHAR reloaded with new search and display fields
NEWS 25	JAN 29	CAS Registry Number crossover limit increased to 300,000 in multiple databases
NEWS 26	FEB 13	CASREACT coverage to be extended
NEWS 27	Feb 15	PATDPASPC enhanced with Drug Approval numbers
NEWS 28	Feb 15	RUSSIAPAT enhanced with pre-1994 records
NEWS 29	Feb 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS 30	Feb 26	MEDLINE reloaded with enhancements
NEWS 31	Feb 26	EMBASE enhanced with Clinical Trial Number field
NEWS 32	Feb 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS 33	Feb 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS 34	Feb 26	CAS Registry Number crossover limit increased from 10,000 to 300,000 in multiple databases

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=> S TGACGTT/SQSN AND SQL<=40
          4785 TGACGTT/SQSN
       7760700 SQL<=40
L1        4785 TGACGTT/SQSN AND SQL<=40

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COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                        37.45      37.87

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=> S L1
L2        2070 L1

=> S L2 AND AY>1994
L3        1481 L2 AND AY>1994

=> s l2 and py<1994
L4          30 L2 AND PY<1994

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L5           30 DUP REM L4 (0 DUPLICATES REMOVED)

=> t l5 bib ab kwic 1-30

L5   ANSWER 1 OF 30  CAPLUS  COPYRIGHT 2007 ACS on STN
AN   2001:741468  CAPLUS
DN   135:299472
TI   Sandwich hybridization for detection of mRNAs using immobilized probe
     arrays
IN   Akitaya, Tatsuo; Mitsuhashi, Masato; Cooper, Allan
PA   Hitachi Chemical Research Center, Inc., USA; Hitachi Chemical Company,
     Ltd.
SO   U.S., 221 pp., Cont.-in-part of U.S. Ser. No. 857,059, abandoned.
     CODEN: USXXAM
DT   Patent
LA   English
FAN.CNT 3
     PATENT NO.          KIND   DATE        APPLICATION NO.         DATE
     ---------------     ----   --------    --------------------    --------
PI   US 6300058           B1    20011009    US 1992-974409          19921112
     WO 9315221           A1    19930805    WO 1993-US977           19930129 <--
         W:  CA, JP, KR, US
         RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
     JP 07506482          T     19950720    JP 1993-512765          19930129
PRAI US 1992-827208       B2    19920129
     US 1992-827975       B2    19920129
     US 1992-857059       B2    19920324
     US 1992-974409       A2    19921112
     WO 1993-US977        W     19930129
AB   The present invention provides a method for detecting and quantifying mRNA
     in a sample.  The mRNA that can be detected has a unique sequence.  The
     method includes immobilizing a first polynucleotide to an insol. support.
     The first polynucleotide has a first sequence that hybridizes to the
     unique sequence on the mRNA.  After immobilization of the first
     polynucleotide, the sample is applied to the insol. support under
     conditions that allow the unique sequence on the mRNA to hybridize with
     the first polynucleotide.  Thereafter, a second polynucleotide is applied
     to the insol. support.  This second polynucleotide has a second sequence
     thereon that hybridizes to a portion of the mRNA other than the unique
     sequence.  The application of the second polynucleotide is performed under
     conditions that allow the second polynucleotide to hybridize with mRNA
     immobilized on said support, if present.  Finally, the amount of the second
     polynucleotide immobilized on the support is measured to provide an
     indication of the amount of mRNA present in the sample.  Polynucleotide
```

immobilized supports and sequences useful in the method are also provided. Use of the method to quantify a number of defined sequences in human cell culture lines is demonstrated. Criteria for the design of probes are also discussed.

RE.CNT 81 THERE ARE 81 CITED REFERENCES AVAILABLE FOR THIS RECORD
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	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	US 6300058	B1	20011009	US 1992-974409	19921112	
	WO 9315221	A1	19930805	WO 1993-US977	19930129	<--
	W: CA, JP, KR, US					
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE					
	JP 07506482	T	19950720	JP 1993-512765	19930129	

IT 115926-18-6, DNA (mouse clone 465 gene junB protein cDNA) 119331-28-1, DNA (mouse clone pcD10 gene c-jun RNA formation factor AP 1 cDNA) 124228-98-4, DNA (mouse gene junD RNA formation factor cDNA) 127830-52-8, DNA (human placenta gene junB) 138389-96-5, DNA (human clone 17 gene junD RNA formation factor cDNA) 150793-75-2 150793-76-3
150793-79-6 150793-82-1 150793-87-6 150793-88-7 150793-89-8
150793-90-1 150793-91-2 150794-35-7 150794-46-0 150794-47-1
150794-49-3 150794-51-7 150794-53-9 150794-61-9 150794-68-6
150794-95-9 150794-96-0 150794-97-1 150794-99-3 150795-00-9
150795-01-0 150795-02-1 150795-09-8 150795-10-1 150795-11-2
150795-12-3 150795-13-4 150795-14-5 150795-15-6 150795-26-9
150795-93-0 150795-96-3 150796-17-1 182085-19-4 197873-87-3
197873-88-4 197873-89-5 197873-90-8 197873-91-9 197873-92-0
197873-93-1 197873-94-2 197873-95-3 197873-96-4 197873-97-5
197873-98-6 197873-99-7 197874-00-3 197874-01-4 197874-02-5
197874-04-7 197874-05-8 197874-06-9 197874-07-0 197874-08-1
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197874-19-4 197874-20-7 197874-21-8 197874-22-9 197874-23-0
197874-24-1 197874-25-2 197874-26-3 197874-27-4 197874-28-5
197874-29-6 197874-30-9 197874-31-0 197874-32-1 197874-33-2
197874-34-3 197874-35-4 197874-36-5 197874-37-6 197874-39-8
197874-44-5 197874-45-6 197874-46-7 197874-47-8 197874-48-9
197874-49-0 197874-50-3 197874-51-4 197874-52-5 197874-53-6
197874-54-7 197874-65-0 197874-66-1 197874-67-2 197874-68-3
197874-69-4 197874-70-7 197874-71-8 197874-72-9 197874-73-0
197874-74-1 197874-75-2 197874-76-3 197874-77-4 197874-78-5
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197874-84-3 197874-85-4 197874-86-5 197874-87-6 197874-88-7
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197874-94-5 197874-95-6 197874-96-7 197874-97-8 197874-98-9
197874-99-0 197875-00-6 197875-01-7 197875-02-8 197875-03-9
197875-04-0 197875-05-1 197875-06-2 197875-07-3 197875-08-4
197875-09-5 197875-10-8 197875-11-9 197875-12-0
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197875-18-6 197875-19-7 197875-21-1 197875-22-2 197875-23-3
197875-24-4 197875-25-5 197875-26-6 197875-27-7 197875-28-8
197875-29-9 197875-30-2 197875-31-3 197875-33-5 197875-34-6
197875-36-8 197875-37-9 197875-38-0 197875-39-1 197875-40-4
197875-41-5 197875-42-6 197875-43-7 197875-44-8 197875-45-9
197875-46-0 197875-47-1 197875-48-2 197875-50-6
197875-52-8 197875-53-9 197875-54-0 197875-55-1 197875-56-2
197875-57-3 197875-59-5 197875-60-8 197875-61-9 197875-62-0
197875-63-1 197875-68-6 197875-69-7 197875-70-0 197875-71-1
197875-72-2 197875-73-3 197875-75-5 197875-76-6 197875-77-7
197875-78-8 197875-79-9 197875-80-2 197875-96-0 197875-97-1
197875-98-2 197875-99-3 197876-00-9 197876-01-0 197876-02-1
197876-04-3 197876-05-4 197876-06-5 197876-07-6 197876-09-8
197876-10-1 197876-11-2 197876-12-3 197876-13-4 197876-14-5
197876-15-6 197876-16-7 197876-18-9 197876-19-0 197876-20-3
197876-21-4 197876-22-5 197876-23-6 197876-24-7 197876-25-8

197876-26-9 198002-19-6 198002-20-9 198002-21-0
RL: PRP (Properties)
(unclaimed sequence; sandwich hybridization for detection of mRNAs using immobilized probe arrays)

L5 ANSWER 2 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1996:717007 CAPLUS
DN 126:2519
TI An enhancer element from the octopine synthase (OCS) gene of T-DNA that functions in monocots and dicots
IN Ellis, Jeff G.; Llewellyn, Daniel J.; Peacock, W. James; Dennis, Elizabeth; Bouchez, David
PA Mycogen Plant Science, Inc., USA
SO U.S., 43 pp., Cont.-in-part of U.S. Ser. No. 11,614,abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	US 5573932	A	19961112	US 1990-525897	19900518	
	ZA 8800319	A	19880928	ZA 1988-319	19880118	<--
	ES 2074435	T3	19950916	ES 1988-300853	19880202	
	JP 63276492	A	19881114	JP 1988-26413	19880205	<--
	CA 1309365	C	19921027	CA 1988-558282	19880205	<--
	US 5290924	A	19940301	US 1993-51006	19930421	
	US 5710267	A	19980120	US 1995-460378	19950602	
	US 5837849	A	19981117	US 1995-459178	19950602	
PRAI	US 1987-11614	B2	19870206			
	US 1987-11904	B2	19870206			
	US 1987-63338	A2	19870615			
	US 1990-525866	B1	19900518			
	US 1990-525897	A1	19900518			

AB A DNA sequence common to the octopine synthase gene and six other genes of T-DNA has been identified as an enhancer element that functions in monocotyledonous and dicotyledonous plants. The element has one or two sequence domains and binds the ocs transcription factor. The element is conserved in tobacco and maize and is also found in the cauliflower mosaic virus 35S promoter. The element was identified by its effect on the level of expression from the maize adh1 promoter. After narrowing the function down to a 16 base-pair palindromic sequence, the role of the sequence was confirmed using a synthetic sequence. The stimulatory effect was somewhat insensitive to distance from the promoter. The element plays in a role in wound induction of gene expression.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	US 5573932	A	19961112	US 1990-525897	19900518	
	ZA 8800319	A	19880928	ZA 1988-319	19880118	<--
	ES 2074435	T3	19950916	ES 1988-300853	19880202	
	JP 63276492	A	19881114	JP 1988-26413	19880205	<--
	CA 1309365	C	19921027	CA 1988-558282	19880205	<--
	US 5290924	A	19940301	US 1993-51006	19930421	
	US 5710267	A	19980120	US 1995-460378	19950602	
	US 5837849	A	19981117	US 1995-459178	19950602	

IT 183972-86-3
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(nucleotide sequence, ocs enhancer element of carnation etched ring virus 35S promoter; enhancer element from octopine synthase (OCS) gene of T-DNA that functions in monocots and dicots)

L5 ANSWER 3 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:619168 CAPLUS

DN 119:219168
TI Immobilized and labeled mRNA-complementary probes for rapidly detecting and quantifying mRNA
IN Akitaya, Tatsuo; Cooper, Allan; Mitsuhashi, Masato
PA Hitachi Chemical Co., Ltd., Japan; Hitachi Chemical Research Center, Inc.
SO PCT Int. Appl., 177 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9315221	A1	19930805	WO 1993-US977	19930129 <--
	W: CA, JP, KR, US				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6300058	B1	20011009	US 1992-974409	19921112
	JP 07506482	T	19950720	JP 1993-512765	19930129
PRAI	US 1992-827208	A2	19920129		
	US 1992-857059	A2	19920324		
	US 1992-974409	A2	19921112		
	US 1992-827975	B2	19920129		
	WO 1993-US977	W	19930129		

AB A highly sensitive, quant. and rapid method for detecting and quantifying mRNA in a sample without the need to purify mRNA from cells is described. A polynucleotide sequence unique to the target mRNA is identified. A computer program for identification of this probe is demonstrated. The probe so identified is immobilized on an insol. support and the sample is incubated with this preparation under hybridization conditions. The nonhybridized components of the sample are washed away and the amount of mRNA immobilized is determined The mRNA may be determined using a labeled 2nd probe or with a nucleic acid stain such as ethidium bromide, yoyo-1, or toto-1. The application of this method to quantification of mRNA for human β2 adrenergic receptor and for various G proteins and jun oncogenes was demonstrated.

PI WO 9315221 A1 19930805

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9315221	A1	19930805	WO 1993-US977	19930129 <--
	W: CA, JP, KR, US				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6300058	B1	20011009	US 1992-974409	19921112
	JP 07506482	T	19950720	JP 1993-512765	19930129

IT 197874-82-1 197874-91-2 197875-50-6 197875-56-2
197875-62-0 197875-68-6 197876-09-8 197876-15-6
RL: USES (Uses)
(PCR primer for Go protein cDNA of rat)
IT 197875-11-9
RL: USES (Uses)
(PCR primer for amplification of Go protein cDNA of rat)

L5 ANSWER 4 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1994:155890 CAPLUS
DN 120:155890
TI Detection of cytomegalovirus (CMV) by PCR
IN Hirai, Kanji; Hironaka, Takashi; Yamaguchi, Masaki; Kita, Hiroshi
PA Iatron Lab, Japan; Takara Shuzo Co
SO Jpn. Kokai Tokkyo Koho, 13 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI JP 05317099 A 19931203 JP 1990-415807 19901228 <--
JP 2000032992 A 20000202 JP 1999-211291 19901228
PRAI JP 1990-415807 A3 19901228
AB A method using a series of oligonucleotide primers and probes to detect cytomegalovirus (CMV) by PCR is disclosed. The method is useful in diagnosis of diseases associated with CMV.
PI JP 05317099 A 19931203 Heisei

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 05317099	A	19931203	JP 1990-415807	19901228 <--
JP 2000032992	A	20000202	JP 1999-211291	19901228

IT 145718-35-0 145718-36-1 145718-37-2 145718-38-3
147307-21-9 147307-22-0
RL: USES (Uses)
(primer, nucleotide sequence of, for detection of cytomegalovirus by PCR)

L5 ANSWER 5 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1994:2262 CAPLUS
DN 120:2262
TI Cloning of 16S rRNA gene of Actinobacillus pleuropneumoniae and the use of gene to diagnosis of A. pleuropneumoniae
IN Nunofuji, Satoshi; Mise, Shizuo; Seto, Yasuhiro; Taneda, Takayuki; Sakano, Tetsuya
PA Nippon Flour Mills, Japan; Nat Federation Agric Coop Ass
SO Jpn. Kokai Tokkyo Koho, 17 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 05219955	A	19930831	JP 1992-26868	19920213 <--

PRAI JP 1992-26868 19920213
AB The 16S rRNA gene of Actinobacillus pleuropneumoniae is cloned and sequenced, and DNA probes designed from the gene for diagnosis of the bacteria which is associated with pig pleuropneumonia. Fragments of the 16S rRNA gene were obtained from the DNA of A. pleuropneumoniae serotype 1, 2, and 5 by PCR using DNA primers derived from the consensus region of known bacterial 16S rRNA gene. The 16S rRNA gene fragments were used to clone the full length 16S rRNA genes (3) from a genomic libraries of A. pleuropneumoniae constructed on λDASH11.
PI JP 05219955 A 19930831 Heisei

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 05219955	A	19930831	JP 1992-26868	19920213 <--

IT 151442-89-6 151442-90-9 151442-91-0 151442-92-1 151442-93-2
151442-94-3 151442-95-4 151442-96-5 151442-97-6
151442-98-7 151442-99-8 151443-00-4 151443-01-5 151443-02-6
151443-03-7 151443-04-8 151443-05-9 151443-06-0 151443-07-1
151443-08-2 151443-09-3 151443-10-6 151443-11-7 151443-12-8
151443-13-9 151443-14-0 151443-15-1 151443-16-2 151443-17-3
151443-18-4 151443-19-5
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, derived from 16S rRNA gene of Actinobacillus pleuropneumoniae, for diagnosis of A. pleuropneumoniae)

L5 ANSWER 6 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1994:2236 CAPLUS
DN 120:2236
TI Cloning of 16S rRNA gene of Pasteurella maltocida and the use of gene to diagnosis of P. maltocida
IN Mise, Shizuo; Nunofuji, Satoshi; Seto, Yasuhiro; Taneda, Takayuki; Sakano, Tetsuya

PA Nippon Flour Mills, Japan; Nat Federation Agric Coop Ass
SO Jpn. Kokai Tokkyo Koho, 14 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 05219954	A	19930831	JP 1992-26867	19920213 <--
PRAI	JP 1992-26867		19920213		

AB The 16S rRNA gene of Pasteurella maltocida is cloned and sequenced, and DNA probes are designed from the gene for diagnosis of the bacteria which is associated with respiratory diseases of livestock. A fragment of the 16S rRNA gene was obtained from the DNA of P. maltocida Kobe6 strain by PCR using DNA primers derived from the consensus region of known bacterial 16S rRNA gene. The 16S rRNA gene fragment was used to clone the full length 16S rRNA gene from a genomic library of P. maltocida Kobe6 constructed on λDASH11.

PI JP 05219954 A 19930831 Heisei

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 05219954	A	19930831	JP 1992-26867	19920213 <--

IT 151442-96-5 151442-97-6 151442-99-8 151443-00-4 151618-03-0
151618-04-1 151618-05-2 151618-06-3 151618-07-4 151618-08-5
151618-09-6 151618-10-9 151618-11-0 151618-12-1 151618-13-2
151618-14-3 151618-15-4 151618-16-5 151618-17-6
151618-18-7 151618-19-8 151618-20-1 151618-21-2 151618-22-3
151618-23-4 151618-24-5 151618-25-6 151618-26-7 151618-27-8
151618-28-9 151618-29-0 151618-30-3 151618-31-4 151618-32-5
151618-33-6 151618-34-7 151618-35-8 151618-36-9
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, derived from 16S rRNA gene of, for diagnosis of Pasteurella maltocida)

L5 ANSWER 7 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:249149 CAPLUS
DN 118:249149
TI Multiple protein-binding domains and functional cis-elements in the 5'-flanking region of the human pyruvate dehydrogenase α-subunit gene
AU Chang, Mei; Naik, Sharon; Johanning, Gary L.; Ho, Lap; Patel, Mulchand S.
CS Sch. Med., Case West. Reserve Univ., Cleveland, OH, 44106, USA
SO Biochemistry (1993), 32(16), 4263-9
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB The 5'-flanking region of the α-subunit gene of the human pyruvate dehydrogenase (E1) was characterized. DNase I footprinting with rat liver nuclear exts. identified 7 major protein-binding domains termed P1 through P7 in a 796 base pair DNA fragment (base pairs -763 to +33). P1 through P4 are clustered in the -221/+33 region. These protein-binding domains contain several known consensus sequences such as a TATA box, CAAT box, Sp1, and CRE, which all have previously been implicated in the constitutive transcription of several genes. Oligonucleotide competition studies indicate that oligonucleotides specific for CTF/NF-1 and Sp1 displaced the nuclear proteins bound to the CAAT box (within P3) and an Sp1 site (within P4), resp. Several other well-characterized and purified transactivators (c-Fos, c-Jun, C/EBP, AP-2, and Sp1) have been shown to bind to the -221/+33 region. Other elements located upstream of the -221/+33 region, which includes nuclease protection domains P5-P7, are required for enhanced promoter activity of the 796 bp sequence. Promoter activity was measured by transient expression of a chloramphenicol acetyltransferase gene ligated to deletion fragments of the 5'-flanking region. Crucial element(s) for promoter activity and complex DNA-nuclear

protein interactions were confined within a region spanning -221/+33. This region also retained more than 75% of the promoter activity of the 796 bp sequence. Addnl., this promoter region shows characteristics of both facultative and housekeeping gene promoters, suggesting complex transcription regulation.

SO Biochemistry (1993), 32(16), 4263-9
CODEN: BICHAW; ISSN: 0006-2960

IT 147758-87-0
RL: BIOL (Biological study)
(cAMP responsive element, of pyruvate dehydrogenase α-subunit gene of human, sequence of)

L5 ANSWER 8 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:642161 CAPLUS
DN 119:242161
TI Nested polymerase chain reaction for detection of Mycobacterium tuberculosis in clinical samples
AU Miyazaki, Yoshitsugu; Koga, Hironobu; Kohno, Shigeru; Kaku, Mitsuo
CS Sch. Med., Nagasaki Univ., Nagasaki, 852, Japan
SO Journal of Clinical Microbiology (1993), 31(8), 2228-32
CODEN: JCMIDW; ISSN: 0095-1137
DT Journal
LA English
AB The nested polymerase chain reaction technique was compared with the conventional smear and culture methods for detection of Mycobacterium tuberculosis. The nested polymerase chain reaction used in this study showed excellent specificity, sensitivity, and agreement with the conventional methods for 417 clin. samples, indicating a contribution to the rapid diagnosis of mycobacterial infectious diseases.
SO Journal of Clinical Microbiology (1993), 31(8), 2228-32
CODEN: JCMIDW; ISSN: 0095-1137
IT 151219-33-9 151219-34-0
RL: USES (Uses)
(nested PCR primer, Mycobacterium tuberculosis detection in clin. samples using)

L5 ANSWER 9 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:421509 CAPLUS
DN 119:21509
TI Detection of 12 germ-line mutations in the adenomatous polyposis coli gene by polymerase chain reaction
AU Ando, Hiroshi; Miyoshi, Yasuo; Nagase, Hiroki; Baba, Shozo; Nakamura, Yusuke
CS Dep. Biochem., Cancer Inst., Tokyo, Japan
SO Gastroenterology (1993), 104(4), 989-93
CODEN: GASTAB; ISSN: 0016-5085
DT Journal
LA English
AB The adenomatous polyposis coli (APC) gene at chromosome 5q21 that is responsible for familial adenomatous polyposis (FAP) was recently isolated, and germ-line mutations in a substantial number of FAP families were characterized. Based on this information, the authors attempted to develop a presymptomatic diagnosis test for members of families that carry FAP. A rapid screening procedure using a polymerase chain reaction (PCR) method without radioisotopes, if necessary, coupled with digestion of restriction enzymes has been performed by detection of germ-line mutations that alter the size of DNA fragments or affect the recognition site of restriction enzymes in the APC locus. A rapid screening procedure to detect germ-line mutations at 12 loci that cause adenomatous polyposis was established. Using these 12 systems, presymptomatic diagnoses can be made with 100% accuracy within 24 h. The procedures will be useful for counseling of members in some FAP families, which accounted for nearly 40% of the 95 FAP kindreds that have been detected by the germ-line mutations so far.

SO Gastroenterology (1993), 104(4), 989-93
CODEN: GASTAB; ISSN: 0016-5085
IT 148267-28-1 148267-29-2 148267-30-5 148267-31-6 148267-32-7
148267-33-8 148267-34-9 148267-35-0 148267-36-1 148267-37-2
148267-38-3 148267-39-4 148267-40-7 148267-41-8 148267-42-9
148267-43-0 148267-44-1 148267-45-2 148267-46-3 148267-47-4
148267-48-5 148267-49-6
RL: USES (Uses)
(PCR primer, for adenomatous polyposis coli gene mutation detection, in human with familial adenomatous polyposis)

L5 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:596771 CAPLUS
DN 119:196771
TI Type differentiation of herpes simplex virus by stringent hybridization of polymerase chain reaction products
AU Inouye, S.; Hondo, R.
CS Dep. Microbiol., Inst. Public Health, Tokyo, Japan
SO Archives of Virology (1993), 129(1-4), 311-16
CODEN: ARVIDF; ISSN: 0304-8608
DT Journal
LA English
AB A simple procedure for type differentiation of herpes simplex virus with the use of polymerase chain reaction (PCR)-amplified DNAs, was established: 1. The target sequence region for PCR was chosen from the coding sequences for an envelope protein, with the terminal sequences for PCR primers to be common among different types, but with the internal sequences to be variable. 2. Biotin-labeled probes for each type were prepared by PCR with the above primers and the templates from standard viruses of different types. 3. With templates from isolated strains or clin. specimens, the target DNA segment was amplified, and then immobilized on microplate wells. 4. Hybridization was carried out with the biotin-probes under a stringent condition so that the immobilized DNA was hybridized only with the homologous-type probe. 5. This hybridization result was visualized by using streptavidin-conjugated peroxidase and coloring reagents. This procedure may be applicable to differentiation of types or strains belonging to a group of closely related viruses.
SO Archives of Virology (1993), 129(1-4), 311-16
CODEN: ARVIDF; ISSN: 0304-8608
IT 150742-48-6 150742-49-7
RL: USES (Uses)
(PCR primer, for herpes simplex virus strain differentiation)

L5 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:426464 CAPLUS
DN 119:26464
TI Functional analysis of rev-responsive element of the human immunodeficiency virus type 1
AU Lee, Hyeong Yeol; Lee, Ann Hwee; Kang, Shin Sung; Sung, Young Chul
CS Dep. Life Sci., Pohang Inst. Sci. Technol., Pohang, S. Korea
SO Han'guk Saenghwa Hakhoechi (1992), 25(3), 236-43
CODEN: KBCJAK; ISSN: 0368-4881
DT Journal
LA Korean
AB Expression of the structural proteins of human immunodeficiency virus type (HIV-1) requires the Rev protein encoded by the rev open reading frame. Rev protein interacts with Rev-responsive element RRE located in the env region of the viral mRNA and seems to mediate the export of the incompletely spliced viral mRNA to the cytoplasm. RRE has a complex secondary structure which is composed of a central stem (I'), a small stem (I) and 5 stem/loops (II, III, IV, V, VI). To investigate which region of RRE is essential for the interaction with Rev protein, mutational anal. in RRE was carried out. The authors examined the nature of the mutated RRE in several assay systems, p24 ELISA assay, reverse transcriptase assay, and

chloramphenicol acetyltransferase assay. Here, the secondary structure of stem/loop II region is critical for the Rev response. Other structural components within RRE RNA seem to have only subsidiary roles. Also, RRE appears to contain a neg. sequence which hinders the expression of structural gene in the absence of the Rev protein.

SO Han'guk Saenghwa Hakhoechi (1992), 25(3), 236-43
CODEN: KBCJAK; ISSN: 0368-4881

IT 147259-46-9 147259-47-0 147259-48-1 147259-49-2 147259-50-5
147302-49-6 147302-50-9 147302-51-0 147302-52-1 147302-53-2
147302-54-3 147302-55-4 147302-56-5 147302-57-6 147302-58-7
147302-59-8 147302-60-1
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(rev protein regulation by, as human immunodeficiency virus response element analog, structure in)

L5 ANSWER 12 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1993:74425 CAPLUS
DN 118:74425
TI Increased sensitivity for detection of human cytomegalovirus in urine by removal of inhibitors for the polymerase chain reaction
AU Yamaguchi, Yuki; Hironaka, Takashi; Kajiwara, Michiko; Tateno, Emiko; Kita, Hiroshi; Hirai, Kanji
CS Dep. Cell Regul., Med. Res. Inst., Tokyo, Japan
SO Journal of Virological Methods (1992), 37(2), 209-18
CODEN: JVMEDH; ISSN: 0166-0934
DT Journal
LA English
AB The presence of inhibitors in urine interferes with the enzymic reaction of the polymerase chain reaction (PCR) for detection of human cytomegalovirus (HCMV). To remove inhibitors, HCMV virions in urine were precipitated with polyethylene glycol, or DNA was extracted from urine by the use of glass powder and subjected to PCR followed by Southern blot hybridization with alkaline phosphatase-linked oligonucleotide probes. These simple, rapid methods increased significantly the sensitivity of PCR for detection of HCMV in urine.
SO Journal of Virological Methods (1992), 37(2), 209-18
CODEN: JVMEDH; ISSN: 0166-0934
IT 145718-35-0 145718-36-1 145718-37-2 145718-38-3
RL: USES (Uses)
(polymerase chain reaction primer, for human cytomegalovirus detection in urine)

L5 ANSWER 13 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1992:1774 CAPLUS
DN 116:1774
TI Detection of transcripts of human papilloma virus in biological samples
IN Hendricks, David A.; Lane, David J.; Rigby, Susan; Parodos, Kyriaki
PA Gene-Trak Systems, USA
SO PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9108312	A1	19910613	WO 1990-US7057	19901203 <--
	W: AU, CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
	AU 9169669	A	19910626	AU 1991-69669	19901203 <--
	EP 502994	A1	19920916	EP 1991-901374	19901203 <--
	EP 502994	B1	19950906		
	R: DE, FR, GB, IT				

	JP 05501650	T	19930402	JP 1991-501759	19901203 <--
	EP 662518	A2	19950712	EP 1995-200344	19901203
	EP 662518	B1	20011107		
	R: DE, FR, GB, IT				
	US 5580970	A	19961203	US 1994-207226	19940304
PRAI	US 1989-444526	A	19891201		
	EP 1991-901374	A3	19901203		
	WO 1990-US7057	A	19901203		
	US 1990-622742	B1	19901205		

AB Methods for the diagnosis and prognosis of infection by human papilloma virus are described. The method uses probes to identify transcription from genes E6 and E7 associated with neoplastic transformation by capture hybridization. Probes are described that are specific for a number of isolates with high oncogenic potential. The design of probes for detection of splices site regions of the mature E6 and E7 transcripts and their use, and the use of capture probes immobilized on magnetic particles are described. The system detected 500 fg of target nucleic acid in a sample. Response of the assay was linear in the range 100 fg to 500 pg.

PI WO 9108312 A1 19910613

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9108312	A1	19910613	WO 1990-US7057	19901203 <--
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
AU 9169669	A	19910626	AU 1991-69669	19901203 <--
EP 502994	A1	19920916	EP 1991-901374	19901203 <--
EP 502994	B1	19950906		
R: DE, FR, GB, IT				
JP 05501650	T	19930402	JP 1991-501759	19901203 <--
EP 662518	A2	19950712	EP 1995-200344	19901203
EP 662518	B1	20011107		
R: DE, FR, GB, IT				
US 5580970	A	19961203	US 1994-207226	19940304

IT 136361-39-2 136361-43-8 136361-45-0 136361-46-1 136361-47-2
136361-48-3 136361-50-7 136361-51-8 136361-52-9
136361-53-0 136361-54-1 136361-56-3 136361-57-4 136361-58-5
136361-59-6 136361-61-0 136361-62-1 136361-63-2 136361-64-3
136361-65-4 136361-66-5 136361-67-6 136361-68-7 136361-69-8
136361-70-1 136361-71-2 136361-72-3 136361-73-4 136361-74-5
136361-75-6 136361-76-7 136361-77-8 136361-78-9 136361-79-0
136361-80-3 136361-81-4 136361-82-5 137748-44-8
RL: BIOL (Biological study)
(oligonucleotide probe for processed transcript of human papilloma gene E6 or E7)

L5 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1992:77829 CAPLUS
DN 116:77829
TI Amplification of nucleic acid sequences
IN Copley, Clive Graham; Anwar, Rashida; Mcpheat, William Leishman; Markham, Alexander Fred; Smith, John Craig
PA Imperial Chemical Industries PLC, UK
SO Eur. Pat. Appl., 45 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 439330	A2	19910731	EP 1991-300479	19910122 <--
EP 439330	A3	19920219		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
AU 9169384	A	19910801	AU 1991-69384	19910116 <--
AU 652548	B2	19940901		

	GB 2240339	A	19910731	GB 1991-1373	19910122 <--
	GB 2240339	B	19940216		
	CA 2034883	A1	19910726	CA 1991-2034883	19910124 <--
	JP 06133800	A	19940517	JP 1991-7996	19910125
PRAI	GB 1990-1764	A	19900125		
	GB 1990-25283	A	19901121		

AB A method for amplification of target nucleic acids for diagnosis or detn.of disease potential, to identify drug resistance sequences, and to detect nucleotide sequence variations in general, is described. The target nucleic acid contains an unknown sequence, a priming region ofknown nucleotide sequence for hybridization with a primer, and a vectorette portion, at least one strand of which has a sequence which in its single- or double-stranded form is capable of blocking hybridization, e.g by being bound by a protein such as a restriction enzyme or a DNA or RNA polymerase. Vectorettes may have a terminal polymerization blocking moiety on one strand with the other strand containing the sequence forming the protein-binding sequence or they may contain a region of noncomplementarity that forms protein-binding sequences for 2 different proteins. The use of the vectorette allows the amplification of a sequence in genomic DNA with limited information about the sequence of interest; a sequence long enough to act as one of the primers is all that is needed. The second primer lies within the vectorette and no extension product is produced if their is no 1st priming region. The method was used to amplify protein and 23S rRNA genes of Chlamydia trachomatis.

PI EP 439330 A2 19910731

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 439330	A2	19910731	EP 1991-300479	19910122 <--
	EP 439330	A3	19920219		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
	AU 9169384	A	19910801	AU 1991-69384	19910116 <--
	AU 652548	B2	19940901		
	GB 2240339	A	19910731	GB 1991-1373	19910122 <--
	GB 2240339	B	19940216		
	CA 2034883	A1	19910726	CA 1991-2034883	19910124 <--
	JP 06133800	A	19940517	JP 1991-7996	19910125

IT 136509-47-2 136509-48-3 136509-87-0 136509-88-1 136509-89-2 136509-90-5

RL: BIOL (Biological study)
(primers for polymerase chain reaction amplification of target vectorette-containing nucleic acids)

L5 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1992:35362 CAPLUS
DN 116:35362
TI ApoB gene nonsense and splicing mutations in a compound heterozygote for familial hypobetalipoproteinemia
AU Huang, Li Shin; Kayden, Herbert; Sokol, Ronald J.; Breslow, Jan L.
CS Lab. Biochem. Genet. Metab., Rockefeller Univ., New York, NY, 10021, USA
SO Journal of Lipid Research (1991), 32(8), 1341-8
CODEN: JLPRAW; ISSN: 0022-2275
DT Journal
LA English
AB Two novel apoB gene mutations were identified in a patient (CM) with phenotypic homozygous hypobetalipoproteinemia. Haplotype anal. of the apoB alleles from this patient and his family members revealed him to be a genetic compound for the disease. In contrast to previous studies of other hypobetalipoproteinemic patients, no clues existed as to where in the apoB gene the mol. defects resided. Therefore, it was necessary to characterize the apoB genes of the patient by sequence anal. The apoB gene contains 29 exons and is 43 kb in length. The gene encodes a 14.1 kb mRNA and a 4563 amino acid protein. Both apoB alleles from the patient were cloned via 26 sets of polymerase chain reactions (PCR). These clones contained a total of .apprx.24 kb of apoB gene sequence, including regions

5' and 3' to the coding region, 29 exons, and the intron/exon junctions. Complete DNA sequence anal. of these clones showed that each apoB allele had a mutation. In the paternal apoB allele, there was a splicing mutation. The first base of the dinucleotide consensus sequence (GT) in the 5' splice donor site in intron 5 was replaced by a T. It is likely that this base substitution interferes with proper splicing and results in the observed absence of plasma apoB. In the maternal apoB allele, there was a nonsense mutation. The first base of the Arg codon (CGA) at residue 412 in exon 10 was replaced by a T, resulting in a termination codon (TGA). The nonsense mutation is likely to terminate translocation after residue 411 resulting in a severely truncated protein only 9% of the length of B-100. The inheritance of these defective apoB alleles cosegregated with low total cholesterol levels observed in family members. One of the siblings, MM, who also presented with phenotypic homozygous hypobetalipoproteinemia, had both defective apoB alleles. Of the 2 other siblings, both of whom were phenotypical heterozygotes for the disease, one (GM) had the allele with the splicing mutation and the other (JM) had the allele with the nonsense mutation. In summary, a strategy is presented for identifying apoB gene mutations by PCR cloning and sequencing. This is useful for anal. of defects in patients where there is no clue as to the location of the mutation. The technique has resulted in the identification of 2 novel apoB gene mutations.

SO Journal of Lipid Research (1991), 32(8), 1341-8
CODEN: JLPRAW; ISSN: 0022-2275

IT 137924-65-3P 137924-75-5P
RL: PREP (Preparation)
(preparation of polymerase chain reaction probe, for identification of polymorphism in apolipoprotein B gene of human)

L5 ANSWER 16 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1991:20613 CAPLUS
DN 114:20613
TI Hybridization method, primers, and probes for detecting bacteria and eukaryotes, especially in food products
IN Allaer, Didier Georges Jean Marie; Rossius, Michel Thierry Jean Francois; Renard, Andre Jean Joseph
PA Societe Europeenne de Biotechnologie, Belg.
SO Fr. Demande, 16 pp.
CODEN: FRXXBL
DT Patent
LA French
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	FR 2636075	A1	19900309	FR 1988-11693	19880907 <--
	FR 2636075	B1	19911115		
PRAI	FR 1988-11693		19880907		

AB Bacteria and eukaryotes (especially yeast, fungi, and parasites) are detected (especially in food products) by extracting rRNA, transcribing the rRNA into DNA with reverse transcriptase, preparing cDNA in the presence of primer(s), and amplifying and detecting the DNA. The rRNA is particularly 16S rRNA or the corresponding rRNA in eukaryotes. Primers and probes from Escherichia coli 16S rRNA are described.

PI FR 2636075 A1 19900309

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	FR 2636075	A1	19900309	FR 1988-11693	19880907 <--
	FR 2636075	B1	19911115		

IT 130938-14-6 130958-35-9 130958-38-2 130958-40-6 130958-42-8
130958-43-9 131092-62-1 131092-64-3
RL: ANST (Analytical study)
(primer or probe of, of Escherichia coli 16S rRNA, for bacteria and eukaryote detection)

L5 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1991:179630 CAPLUS
DN 114:179630
TI Cytoplasmic and periplasmic expression of a synthetic gene for ferredoxin in Escherichia coli
AU Bourdineaud, J. P.; Howard, S. P.; Pages, J. M.; Bernadac, A.; Leroy, G.; Bruschi, M.; Lazdunski, C.
CS Cent. Biochim. Biol. Mol., Marseille, 13402, Fr.
SO Biochimie (1990), 72(6-7), 407-15
CODEN: BICMBE; ISSN: 0300-9084
DT Journal
LA English
AB A synthetic gene coding for a modified ferredoxin II of Desulfovibrio desulfuricans Norway strain was assembled from 10 olgionucleotides. This gene was cloned into various expression vectors allowing either cytoplasmic expression or export to the periplasmic space. In the latter case, 2 different constructs were made, each of which contained the OmpA signal peptide: one of these constructs contained 3 addnl. N-terminal amino acids as compared to the wild-type ferredoxin (56 amino acid residues). The expression of proteins encoded by the 3 constructs was assayed in E. coli and the proteins were localized by cell fractionation and immunogold labeling. A low percentage of the periplasmic ferredoxin (≈5%) was secreted to the medium in the absence of cell lysis. The recombinant ferredoxin was purified and found to be correctly processed by the leader peptidase. However, due to the high cysteine content intramol. and intermol. disulfide bonds were formed and prevented binding of [4Fe-4S] clusters.
SO Biochimie (1990), 72(6-7), 407-15
CODEN: BICMBE; ISSN: 0300-9084
IT 133335-33-8 133335-37-2 133335-38-3 133335-39-4 133335-41-8
133335-42-9 133335-43-0 133335-44-1 133335-50-9
133335-52-1
RL: PROC (Process)
(synthesis and ligation of, for assembly of synthetic gene for modified apoferredoxin II of Desulfovibrio desulfuricans)

L5 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1990:113598 CAPLUS
DN 112:113598
TI Synthetic gene coding cystatin α and its use for manufacturing the same
IN Ike, Yoshimasa; Katsunuma, Nobuhiko
PA Mitsui Toatsu Chemicals, Inc., Japan
SO Jpn. Kokai Tokkyo Koho, 7 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 64002582	A	19890106	JP 1987-290697	19871119 <--
PRAI JP 1987-21706	A1	19870203		

AB Gene encoding cystatin α(I) is synthesized, cloned, and expressed in recombinant Escherichia coli. D. Plasmid pTP1-E010 containing I gene was transformed into E. coli MC 1061. The E. coli transformants were cultured overnight at 37°in 5 mL L broth containing yeast extract, trypton, and salt to produce 200-250 ng I/mL/A 600 nm determined by EIA method or 180-230 ng I/mL/A 600 nm determined by papain inhibition method.
PI JP 64002582 A 19890106 Showa

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 64002582	A	19890106	JP 1987-290697	19871119 <--

IT 118899-71-1 118899-84-6 118899-94-8 118899-95-9 118899-97-1

118899-98-2 118899-99-3 118900-00-8 118900-02-0
118900-03-1 118900-04-2 118900-05-3 118900-06-4
118900-07-5 118900-08-6 118900-09-7 118900-10-0 118900-12-2
118900-14-4
RL: PRP (Properties)
(synthetic DNA fragment of cystatin α gene)

L5 ANSWER 19 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1990:510491 CAPLUS
DN 113:110491
TI Ruthenium-containing DNA and RNA for use in nucleic acid sequencing and hydridization
IN Bannwarth, Wilhelm; Knorr, Reinhard; Mueller, Francis; Schmidt, Dieter
PA Hoffmann-La Roche, F., und Co. A.-G., Switz.
SO Eur. Pat. Appl., 16 pp.
CODEN: EPXXDW
DT Patent
LA German
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	EP 340605	A2	19891108	EP 1989-107439	19890425	<--
	EP 340605	A3	19910508			
	R: BE, CH, DE, ES, FR, GB, IT, LI, NL, SE					
	AU 8933343	A	19891109	AU 1989-33343	19890424	<--
	AU 622899	B2	19920430			
	JP 02011597	A	19900116	JP 1989-107096	19890426	<--
PRAI	CH 1988-1662	A	19880504			
	CH 1988-3171	A	19880826			

AB DNA or RNA covalently bound to a Ru complex is prepared These derivs. may be used in nucleic acid hybridization analyses and in sequencing. An activated Ru complex was prepared by reaction of Ru[batho]2[batho(CH2)5CO2H]Cl2 with 1,1,3,3-tetramethyl-2-succinimdyluronium tetrafluoroborate. A 5'-amino-oligodeoxyribonucleotide (a 25-mer) was reacted with the activated complex to prepare a Ru-labeled primer which was used in DNA sequencing by the Sanger method.
PI EP 340605 A2 19891108

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	EP 340605	A2	19891108	EP 1989-107439	19890425	<--
	EP 340605	A3	19910508			
	R: BE, CH, DE, ES, FR, GB, IT, LI, NL, SE					
	AU 8933343	A	19891109	AU 1989-33343	19890424	<--
	AU 622899	B2	19920430			
	JP 02011597	A	19900116	JP 1989-107096	19890426	<--

IT 7440-18-8DP, Ruthenium, complexes, nucleic acid conjugates 119572-76-8P
119572-77-9P 119572-78-0P 119572-79-1P 119572-80-4P
119572-81-5P 119592-95-9P
RL: PREP (Preparation)
(preparation of, for nucleic acid hybridization and sequencing)
IT 119509-29-4 119509-34-1 119509-35-2 119509-37-4
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction of, with activated ruthenium complex)

L5 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1990:135577 CAPLUS
DN 112:135577
TI Method and device for improved restriction fragment length polymorphism analysis
IN Helentjaris, Timothy George; Lee, Mark S.; Shattuck-Eidens, Donna Marie
PA Native Plants, Inc., USA
SO Eur. Pat. Appl., 27 pp.
CODEN: EPXXDW
DT Patent

LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 317239	A2	19890524	EP 1988-310729	19881114 <--
	EP 317239	A3	19900117		
	R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
	JP 02002400	A	19900108	JP 1988-287487	19881114 <--
	JP 2634208	B2	19970723		
	CA 1323553	C	19931026	CA 1988-583057	19881114 <--
	US 5324631	A	19940628	US 1991-752907	19910826
PRAI	US 1987-120309	A	19871113		
	US 1988-266970	A	19881103		

AB A method for rapid restriction fragment length polymorphism (RFLP) anal. comprises (a) hybridizing a restricted target DNA sample and fluorescent mol.-labeled oligodeoxyribonucleotide(s) which is complementary to a portion of the RFLP in the presence of an oligodeoxyribonucleotide elongating enzyme; (b) separating the hybridization mixture by PAGE; and (c) exciting and detecting any fluorescing mols in the gel. Variations in nucleic acid sequence between ≥2 nucleic acid test samples are detected by an enhancement step using a polymerase chain reaction (PCR) technique and detecting the enhancement products of the hybridization mixture An apparatus for detecting the fluorescing mols. in the gel in also disclosed. Maize loci 288 and 451 of different maize cultivars were analyzed using 2 sets of primers and PCR amplification between the primers with Taq polymerase. The amplified DNA was sequenced using a Sequenase kit (U.S. Biochem. Corp.); the sequences are presented.

PI EP 317239 A2 19890524

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 317239	A2	19890524	EP 1988-310729	19881114 <--
	EP 317239	A3	19900117		
	R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
	JP 02002400	A	19900108	JP 1988-287487	19881114 <--
	JP 2634208	B2	19970723		
	CA 1323553	C	19931026	CA 1988-583057	19881114 <--
	US 5324631	A	19940628	US 1991-752907	19910826

IT 125855-48-3 125855-54-1 125855-59-6 125855-76-7
125855-79-0 125901-83-9
RL: ANST (Analytical study)
(as primer in restriction fragment length polymorphism anal., of different maize cultivars)

L5 ANSWER 21 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1989:627755 CAPLUS
DN 111:227755
TI Unique substrate specificity and regulatory properties of PKC-ε: a rationale for diversity
AU Schaap, Dick; Parker, Peter J.; Bristol, Andrew; Kriz, Ron; Knopf, John
CS Ludwig Inst. Cancer Res., London, UK
SO FEBS Letters (1989), 243(2), 351-7
CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB Protein kinase C (PKC)-ε was isolated from a murine brain cDNA library. The clone, λ61PKC-ε, encoded a polypeptide of 737 amino acids that is homologous to other PKCs. Northern anal. showed that the 7 kb mRNA for this cDNA is widely expressed. The protein, when expressed in COS-1 cells, displayed phorbol ester-binding activity. However in order to detect the kinase activity of PKC-ε, it was necessary to employ a synthetic peptide substrate based upon the pseudosubstrate site. Subsequent anal. demonstrated that PKC-ε, while showing certain properties characteristic of the PKC family, has a quite distinct substrate specificity and is independent of Ca2+.

SO FEBS Letters (1989), 243(2), 351-7
CODEN: FEBLAL; ISSN: 0014-5793
IT 120298-88-6P
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation and cDNA library screening for protein kinase C-ε sequences using)

L5 ANSWER 22 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1990:1993 CAPLUS
DN 112:1993
TI Bathophenanthroline-ruthenium(II) complexes as nonradioactive labels for dideoxy DNA sequencing
AU Bannwarth, Willi
CS Cent. Res. Units, F. Hoffmann-La Roche Ltd., Basel, CH-4002, Switz.
SO Analytical Biochemistry (1989), 181(2), 216-19
CODEN: ANBCA2; ISSN: 0003-2697
DT Journal
LA English
AB Bathophenanthroline-Ru(II) complexes represent interesting nonradioactive label mols. which can be measured in a time-resolved mode with high sensitivity. This report demonstrates that Ru complex-labeled primers can be applied in dideoxy sequencing protocols giving the same sequencing patterns as unlabeled primers.
SO Analytical Biochemistry (1989), 181(2), 216-19
CODEN: ANBCA2; ISSN: 0003-2697
IT 119509-37-4P 123996-97-4P 124024-70-0P
RL: PREP (Preparation)
(preparation of, as universal primer for M13 dideoxy DNA sequencing)

L5 ANSWER 23 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1990:49710 CAPLUS
DN 112:49710
TI Regulation of fos gene: a paradigm for nuclear oncogenes
AU Verma, I. M.; Visvader, J.; Lamph, W. W.; DeTogni, P.; Barber, J.; Sassone-Corsi, P.
CS Salk Inst., San Diego, CA, 92138, USA
SO UCLA Symposia on Molecular and Cellular Biology, New Series (1989), 87(Gene Transfer Gene Ther.), 129-49
CODEN: USMBD6; ISSN: 0735-9543
DT Journal
LA English
AB Proto-oncogene fos is an inducible gene. Expression is invariably very rapid but transient. A cAMP responsive element (CRE) has been identified to be localized between positions -57 to -63 upstream of the 5'-cap site. In DNaseI footprint anal., purified CRE binding protein protects this region. The c-fos cDNA is able to induce transformation if an A-T rich stretch located downstream of the coding domain is removed. Both the viral and cellular fos protein are extensively modified with serine phosphorylation as the predominant modification. Fos monoclonal antibodies have been generated. Regulation of the fos gene is complex, but appears to involve controls at the level of transcription, post-transcription and post-translation.
SO UCLA Symposia on Molecular and Cellular Biology, New Series (1989), 87(Gene Transfer Gene Ther.), 129-49
CODEN: USMBD6; ISSN: 0735-9543
IT 124539-96-4
RL: PROC (Process)
(of gene c-fos promoter, of human, structure and regulation of)

L5 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1990:492125 CAPLUS
DN 113:92125
TI Nucleotide sequences of the Erwinia chrysanthemi ogl and pelE genes negatively regulated by the kdgR gene product

AU Reverchon, Sylvie; Huang, Yue; Bourson, Claude; Robert-Baudouy, Janine
CS Lab. Genet. Mol. Microorg., Inst. Natl. Sci. Appl., Villeurbanne, 69621, Fr.
SO Gene (1989), 85(1), 125-34
CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB The nucleotide sequences of the coding and regulatory regions of the genes encoding oligogalacturonate lyase (OGL) and pectate lyase isoenzyme (PLe) from E. chrysanthemi 3937 were determined The ogl sequence contains an open reading frame (ORF) of 1164 bp coding for a 388-amino acid (aa) polypeptide with a predicted Mr of 44,124. A possible transcriptional start signal showing homol. with the Escherichia coli promoter consensus sequence was detected. In addition, a sequence 3' to the coding region was found to be able to form a secondary structure which may function as an Rho-independent transcriptional termination signal. For the pelE sequence, a long ORF of 1212 bp coding for a 404-aa polypeptide was detected. PLe is secreted into the external medium by E. chrysanthemi, and a potential signal peptide sequence was identified in the pelE gene. In the 5' upstream pelE coding region, a putative promoter resembling E. coli promoter consensus sequences was detected. Furthermore, the region immediately 3' to the pelE translational stop codon may function as an Rho-independent translational termination signal. In strain 3937, the synthesis of OGL and PLe, as well as the other enzymes involved in the pectin-degradative pathway (particularly the kdgT product), are known to be regulated by the KdgR repressor, which mediates galacturonate and polygalacturonate induction. Synthesis of these enzymes is also regulated by the CRP-cAMP complex which mediates catabolite repression. Anal. of the regulatory regions of ogl and pelE allowed to identify possible CRP-binding sites for these 2 genes. Furthermore, comparative study of the regulatory regions of the ogl, kdgT and pelE genes revealed the existence of a highly conserved sequence which could correspond to a whole or partial KdgR-binding site.
SO Gene (1989), 85(1), 125-34
CODEN: GENED6; ISSN: 0378-1119
IT 128513-23-5 128513-24-6 128513-25-7 128513-26-8 128513-38-2 128513-39-3 128907-65-3, Deoxyribonucleic acid (Erwinia chrysanthemi clone pOGL10 gene ogl) 128907-66-4, Deoxyribonucleic acid (Erwinia chrysanthemi clone pPLeD1 gene pelE)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

L5 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1989:188622 CAPLUS
DN 110:188622
TI Bathophenanthroline-ruthenium(II) complexes as non-radioactive labels for oligonucleotides which can be measured by time-resolved fluorescence techniques
AU Bannwarth, Willi; Schmidt, Dieter; Stallard, Robert L.; Hornung, Claudia; Knorr, Reinhard; Mueller, Francis
CS Cent. Res. Units, F. Hoffmann-La Roche and Co. Ltd., Basel, CH-4002, Switz.
SO Helvetica Chimica Acta (1988), 71(8), 2085-99
CODEN: HCACAV; ISSN: 0018-019X
DT Journal
LA English
AB The specific attachment of bathophenanthroline-ruthenium(II) complexes as nonradioactive label mols. to synthetically 5'-NH2-modified oligonucleotides is described. After excitation by light pulses, the fluorescence of these labels can be measured by a time-resolved mode with high sensitivity. No quenching takes place due to coupling of the Ru complexes to the DNA. Ru-complex-labeled oligonucleotides still hybridize specifically to cDNA sequences, and no quenching is observed in the course of the hybridization process.

SO Helvetica Chimica Acta (1988), 71(8), 2085-99
CODEN: HCACAV; ISSN: 0018-019X
IT 119509-29-4P 119509-34-1P 119509-35-2P 119509-36-3P
119509-37-4P
RL: PREP (Preparation)
(preparation of and reaction with bathophenanthroline-ruthenium complexes)
IT 119572-76-8P 119572-77-9P 119572-78-0P 119572-79-1P
119572-80-4P 119572-81-5P 119572-82-6P 119592-95-9P
RL: PREP (Preparation)
(preparation of, as label for nucleic acid hybridization assay with time-resolved fluorescence detection)

L5 ANSWER 26 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1989:434408 CAPLUS
DN 111:34408
TI Total synthesis of the cystatin α gene and its expression in E. coli
AU Katunuma, Nobuhiko; Yamato, Masayuki; Kominami, Eiki; Ike, Yoshimasa
CS Inst. Enzyme Res., Univ. Tokushima, Tokushima, 770, Japan
SO FEBS Letters (1988), 238(1), 116-18
CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB A gene encoding cystatin α was chemical synthesized, cloned, and expressed in E. coli. The gene of 318 base pairs was assembled by enzymic ligation of 19 oligonucleotides and cloned into a pBR322-derived expression plasmid downstream of the tac promoter. The expression product of the synthetic gene was purified by Sephadex G-50 column chromatog. and shown to have the same properties as those of the authentic protein isolated from rat epidermis.
SO FEBS Letters (1988), 238(1), 116-18
CODEN: FEBLAL; ISSN: 0014-5793
IT 118899-71-1 118899-84-6 118899-94-8 118899-95-9 118899-97-1
118899-98-2 118899-99-3 118900-00-8 118900-02-0
118900-03-1 118900-04-2 118900-05-3 118900-06-4
118900-07-5 118900-08-6 118900-09-7 118900-10-0 118900-12-2
118900-14-4
RL: RCT (Reactant); RACT (Reactant or reagent)
(oligonucleotide coupling reaction of)

L5 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1988:493524 CAPLUS
DN 109:93524
TI An automated DNA synthesizer employing deoxynucleoside 3'-phosphoramidites
AU Horvath, Suzanna J.; Firca, Joseph R.; Hunkapiller, Tim; Hunkapiller, Michael W.; Hood, Leroy
CS Div. Biol., California Inst. Technol., Pasadena, CA, 91125, USA
SO Methods in Enzymology (1987), 154(Recomb. DNA, Pt. E), 314-26
CODEN: MENZAU; ISSN: 0076-6879
DT Journal
LA English
AB An automated synthesizer which employs activated deoxynucleoside 3'-phosphoramidites in the solid-phase synthesis of oligodeoxynucleotides is presented. The design of the apparatus, as well as reagents, conditions, and reaction steps are discussed.
SO Methods in Enzymology (1987), 154(Recomb. DNA, Pt. E), 314-26
CODEN: MENZAU; ISSN: 0076-6879
IT 78169-78-5P 115832-20-7P 115832-21-8P 115832-22-9P 115832-23-0P
115832-24-1P 115832-25-2P 115832-26-3P 115832-27-4P
115832-28-5P 115832-29-6P 115832-30-9P 115832-31-0P 115832-32-1P
115832-33-2P 115832-37-6P 115832-43-4P 115832-45-6P 115832-48-9P
115832-49-0P 115832-50-3P 115832-60-5P 115832-63-8P 115832-65-0P
115832-66-1P 115832-67-2P 115832-68-3P 115832-69-4P 115832-70-7P
115832-71-8P 115832-83-2P 115832-84-3P 115832-85-4P 115832-92-3P
115832-93-4P 115832-94-5P 115832-95-6P 115865-63-9P 115973-60-9P

115973-61-0P 115973-62-1P 115973-63-2P 115973-64-3P
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation of, automated synthesizer method for)

L5 ANSWER 28 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1986:16087 CAPLUS
DN 104:16087
TI Gene technology method for producing human γ-interferon and an agent for performing this method
IN Engels, Joachim; Leineweber, Michael; Uhlmann, Eugen; Ulmer, Wolfgang
PA Hoechst A.-G. , Fed. Rep. Ger.
SO Ger. Offen., 26 pp.
CODEN: GWXXBX
DT Patent
LA German
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	DE 3409966	A1	19850926	DE 1984-3409966	19840319	<--
	EP 155590	A2	19850925	EP 1985-102499	19850306	<--
	EP 155590	A3	19870422			
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE					
	HU 37651	A2	19860123	HU 1985-932	19850313	<--
	FI 8501037	A	19850920	FI 1985-1037	19850315	<--
	DK 8501219	A	19850920	DK 1985-1219	19850318	<--
	NO 8501065	A	19850920	NO 1985-1065	19850318	<--
	AU 8540047	A	19850926	AU 1985-40047	19850318	<--
	AU 576226	B2	19880818			
	JP 60210996	A	19851023	JP 1985-52577	19850318	<--
	ES 541350	A1	19851216	ES 1985-541350	19850318	<--
	ZA 8501992	A	19860827	ZA 1985-1992	19850318	<--
PRAI	DE 1984-3409966	A	19840319			

AB A synthetic gene is used in the production of human γ-interferon. The gene is prepared in the form of fragments containing 18-33 nucleotides which are ligated enzymically with phage T4 DNA ligase to produce 3 partial sequences. These are incorporated into hybrid plasmids, amplified in Escherichia coli K12, reisolated, and coupled enzymically to form the complete gene which is incorporated into plasmid pKK177.3 or pMX2 for expression in E. coli.

PI DE 3409966 A1 19850926

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	DE 3409966	A1	19850926	DE 1984-3409966	19840319	<--
	EP 155590	A2	19850925	EP 1985-102499	19850306	<--
	EP 155590	A3	19870422			
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE					
	HU 37651	A2	19860123	HU 1985-932	19850313	<--
	FI 8501037	A	19850920	FI 1985-1037	19850315	<--
	DK 8501219	A	19850920	DK 1985-1219	19850318	<--
	NO 8501065	A	19850920	NO 1985-1065	19850318	<--
	AU 8540047	A	19850926	AU 1985-40047	19850318	<--
	AU 576226	B2	19880818			
	JP 60210996	A	19851023	JP 1985-52577	19850318	<--
	ES 541350	A1	19851216	ES 1985-541350	19850318	<--
	ZA 8501992	A	19860827	ZA 1985-1992	19850318	<--

IT 99402-33-2P 99402-36-5P 99402-37-6P 99402-39-8P 99402-40-1P
99402-41-2P 99402-42-3P 99402-43-4P 99402-44-5P 99402-45-6P
99402-46-7P 99402-47-8P 99402-48-9P 99402-49-0P 99402-50-3P
99402-51-4P 99402-52-5P 99402-53-6P 99402-54-7P 99402-55-8P
99402-56-9P 99402-57-0P 99402-58-1P 99402-59-2P 99402-60-5P
99402-61-6P 99402-62-7P 99402-63-8P 99402-64-9P 99402-66-1P
99402-67-2P 99402-68-3P 99402-69-4P 99402-70-7P
RL: PREP (Preparation)

(preparation of, in human γ-interferon gene synthesis)

L5 ANSWER 29 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1984:630936 CAPLUS
DN 101:230936
TI Improved synthesis of oligodeoxyribonucleotides by solid-phase phosphotriester method utilizing O6-[2-(p-nitrophenyl)ethyl]-2'-deoxyguanosine derivatives
AU Chollet, Andre; Ayala, Edgar; Kawashima, Eric H.
CS Dep. Chem., Biogen S. A., Geneva, CH-1211, Switz.
SO Helvetica Chimica Acta (1984), 67(5), 1356-64
CODEN: HCACAV; ISSN: 0018-019X
DT Journal
LA English
AB The synthesis of oligodeoxyribonucleotides was carried on a cross-linked polystyrene solid support utilizing stable mono- and dinucleotide phosphotriester building blocks. The use of O6-[2-(p-nitrophenyl)ethyl]-2'-deoxyguanosine derivs. gave cleaner DNA fragments by suppressing side reactions. Oligodeoxyribonucleotides ranging from 6-41 bases in length were prepared Modifications improving the phosphotriester method are presented. The purification methods and anal. of synthetic oligodeoxyribonucleotides are described.
SO Helvetica Chimica Acta (1984), 67(5), 1356-64
CODEN: HCACAV; ISSN: 0018-019X
IT 93130-35-9P 93229-31-3P 93229-35-7P 93229-39-1P
93229-43-7P 93229-47-1P 93357-06-3P
RL: SPN (Synthetic preparation); PREP (Preparation)
(solid-phase phosphotriester preparation of, [(nitrophenyl)ethyl]deoxyguanosine derivative as reactant in)

L5 ANSWER 30 OF 30 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1982:486242 CAPLUS
DN 97:86242
TI Rat kappa-chain J-segment genes: two recent gene duplications separate rat and mouse
AU Sheppard, Haynes W.; Gutman, George A.
CS Coll. Med., Univ. California, Irvine, CA, 92717, USA
SO Cell (Cambridge, MA, United States) (1982), 29(1), 121-7
CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB DNA segments containing the Jκ genes from LOUVAIN rat liver were cloned and their nucleotide sequence determined Seven readily identifiable Jκ-coding regions (6 expressible) are evident in the rat, compared with 5 in the mouse (4 expressible). The 2 addnl. J segments in the rat appear to be the result of 2 sequential gene duplications occurring since the divergence of rats and mice. The 1st involved a homologous but unequal crossing-over in a 14-base pair (bp) region spanning the 3' end of the coding region of J1 and J2. The 2nd involved a crossing-over following unequal pairing of the 2 newly duplicated regions. Perhaps the probability of a 2nd duplication was greatly increased following the 1st as a result of the increased target for unequal pairing (370 bp of good homol. vs. 27 bp in the original pairing). Comparisons of rat and mouse J genes show a surprisingly high degree of sequence conservation, both inside and outside the coding regions, similar to the pattern reported previously for the kappa constant-region gene. This provides addnl. evidence that constraints exist on the nucleotide sequences of these genes independent of the function of the encoded proteins.
SO Cell (Cambridge, MA, United States) (1982), 29(1), 121-7
CODEN: CELLB5; ISSN: 0092-8674
IT 82785-01-1 82785-02-2 82785-03-3 82785-04-4 82785-05-5
82785-06-6 82785-07-7
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

3+10.sup.9 D1210 cells by electroporation. The transformed cells.
. .
DETD . . . was phenolchloroform extracted and ethanol precipitated in the presence of 10 ug of yeast tRNA, pelleted, washed, and dried. The nucleic acid pellet was dissolved in 5 ul of water and used to transform 3+10.sup.9 [2+10.sup.9 on second execution] D1210 cells by. . .
DETD . . . pEP1304 with rav.
pEP1400 to
pEP1200 series plasmids with HIV 353-369
pEP1499 substituted for Right Symmetrized Targets.
pEP1500 to
pEP1400 series plasmids containing
pEP1599 modified rav.sub.R genes producing Rav.sub.r proteins
that complement the rav.sub.L.sup.- VF55 mutation.
pEP1600 to
pEP1400 series plasmids containing
pEP1699 modified rav.sub.R genes producing Rav.sub.R proteins
that complement the rav.sub.L.sup.- FW58 mutation.
pEP2000 pEP1009 with rav replaced by arc.
pEP2001 pEP2000 with arc. . .
DETD . . . of DNA binding sites by regulatory proteins: the LexA protein and the arginine repressor use different strategies for functional specificity", Nucleic Acids Research (1988), 16:5089-5105.
DETD HIPP89: Hippel, P H von, and O G Berg, "DNA-Protein Interactions in the Regulation of Gene Expression", pp.1-18 in Protein-Nucleic Acid Interaction. W Saenger and U. Heinemann, Editors. CRC Press, Inc., Boca Raton, Fla. 1989.
DETD . . . M J N Lamerichs, "NMR Studies of Protein-DNA Recognition. The Interaction of LAC Repressor Headpiece with Operator DNA", pp.35-60 in Protein-Nucleic Acid Interaction. W Saenger and U. Heinemann, Editors. CRC Press, Inc., Boca Raton, Fla. 1989.
DETD . . . E, D K Hawley, R Entriken, and W R McClure, "Escherichia coli promoter sequences predict in vitro RNA polymerase selectivity", Nucleic Acids Research (1984), 12:789-800.
DETD . . . and S W Glover, "Basis for changes in DNA recognition by the EcoR124 and EcoR124/3 type I DNA restriction and modification enzymes", J Mol Biol (Jan 1989), 205(1)115-125.
DETD SAEN83: Saenger, W, Principles of Nucleic Acid Structure, Springer Verlag, New York, 1983.
DETD TABO87: Tabor, S, and C C Richardson, "DNA sequence analysis with a modified bacteriophage T7 DNA polymerase", Proc Natl Acad Sci USA (1987), 84:4767-4771.
DETD . . . W F Anderson, and B W Matthews, "The Structure of Cro Repressor Protein", pp.234-263, In: Biological Macromolecules and Assemblies: Volume 2-Nucleic Acids and Interactive Proteins., John Wiley and Sons, Inc., 1985.

=> d his

(FILE 'HOME' ENTERED AT 16:33:52 ON 13 MAR 2007)

FILE 'REGISTRY' ENTERED AT 16:34:58 ON 13 MAR 2007
L1 4785 S TGACGTT/SQSN AND SQL<=40

FILE 'CAPLUS, USPATFULL' ENTERED AT 16:39:23 ON 13 MAR 2007
L2 2070 S L1
L3 1481 S L2 AND AY>1994
L4 30 S L2 AND PY<1994
L5 30 DUP REM L4 (0 DUPLICATES REMOVED)
L6 98885 S ANTISENSE
L7 0 S NUCLEIC ADJ ACID

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L8       314623 S NUCLEIC (W) ACID
L9      1112804 S NUCLEIC (W) ACID OR ODN OR OLIGONUCLEOTIDE OR DNA
L10     3875784 S STABILIZE OR STABILIZED OR MODIFIED OR MODIFICATION
L11        5419 S UNMETHYLATED
L12      799416 S CANCER OR TUMOR OR TUMOUR
L13      695809 S BACTERIA OR BACTERIAL
L14        1142 S L8 AND L10 AND L11 AND L12 AND L6
L15           3 S L14 AND PY<1994
L16           3 DUP REM L15 (0 DUPLICATES REMOVED)

=> s l9 and l10 and l11
L17       2595 L9 AND L10 AND L11

=> s l17 and py<1994
L18        104 L17 AND PY<1994

=> dup rem l18
PROCESSING COMPLETED FOR L18
L19         103 DUP REM L18 (1 DUPLICATE REMOVED)

=> t l19 bib ab kwic 1-20

L19  ANSWER 1 OF 103  USPATFULL on STN
AN     1999:163444  USPATFULL
TI     Introns and exons of the cystic fibrosis gene and mutations thereof
IN     Tsui, Lap-Chee, Toronto, Canada
       Rommens, Johanna M., Willowdale, Canada
       Kerem, Bat-sheva, Jerusalem, Israel
PA     HSC Research Development Corporation, Toronto, Canada (non-U.S.
       corporation)
PI     US 6001588              19991214
       WO 9110734  19910725                                          <--
AI     US 1992-890609          19920713 (7)
       WO 1991-CA9             19910111
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PRAI   CA 1990-2007699     19900110
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DT     Utility
FS     Granted
EXNAM  Primary Examiner: Wax, Robert A.; Assistant Examiner: Lau, Kawai
LREP   Bell Seltzer Intellectual Property Law Group of Alston & Bird LLP
CLMN   Number of Claims: 9
ECL    Exemplary Claim: 1
DRWN   58 Drawing Figure(s); 45 Drawing Page(s)
LN.CNT 5304
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The identification, isolation and cloning of DNA sequences
       coding for mutant forms of the cystic fibrosis gene and their gene
       product are described. DNA sequence information and
       information relating to the genomic structure of the cystic fibrosis
       gene are provided. The mutant forms of the CF gene include specific
       sequence alterations in coding portions or of other genetic information
       at exon/intron boundaries and altered RNA transcripts and mutant protein
       products. Such DNA and protein information is useful in
       developing DNA or protein diagnosis for CF mutations, carrier
       and patient screening, as well as cloning of mutant genes and
       manufacturing of their proteins for investigation into therapies for
       cystic fibrosis.
PI     US 6001588              19991214
       WO 9110734  19910725                                          <--
AB     The identification, isolation and cloning of DNA sequences
       coding for mutant forms of the cystic fibrosis gene and their gene
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